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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/674,277	02/13/2001	Dominique Therese Marie Frechon	P66034US0	5117

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EXAMINER

DUFFY, PATRICIA ANN

ART UNIT	PAPER NUMBER
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1645

DATE MAILED: 06/21/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

**Office Action Summary**

Application No.

09/674,277

Applicant(s)

FRECHON ET AL.

Examiner

Patricia A. Duffy

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 27 December 2004.
- 2a) ☒ This action is **FINAL**.                      2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 20-25 and 27-60 is/are pending in the application.
- 4a) Of the above claim(s) 31-60 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 20-25 and 27-30 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
a) ☐ All    b) ☐ Some \*    c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)  | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                                   | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)             |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>sequence attachments</u> .             |

### RESPONSE TO AMENDMENT

The amendments to the claims filed on 5-12-04 and 12-27-04 have been entered into the record. The amendment to the specification filed on 7-12-04 has been entered into the record. The responses filed 5-12-04, 7-12-04 and 12-27-04 have been entered into the record. Claims 1-19 and 26 have been cancelled. Claims 20-25, and 27-60 are pending.

The text of Title 35 of the U.S. Code not reiterated herein can be found in the previous office action.

### *Election/Restrictions*

Upon reconsideration of the lack of unity, and the fact that the individual SEQ ID NOS: 1 and 2 were examined in the first office action on the merits, Groups I -III are hereby rejoined. The lack of unity with respect to the corresponding method claims and primer pairs is maintained in view that these lack unity of invention in light of the art maintained. The traversal is on the ground(s) that the cited reference no longer anticipates claim 20 and as such, the claims now have unity of invention. This is not found persuasive because the deletion of "insertion" does not remove the art because "mutation" or "substitution" as it is still recited in the claims, broadly encompasses substitutions, insertions and deletions. Substitutions base X could be X for X+1, 2, 3... resulting in a substitution of a single base for multiple replacements or substitution of bases XYZ could be substituted with XZ resulting in the loss of a single or multiple bases and the "consisting of language" does not limit the claims to shorter fragments because a nucleic acid that is larger can also specifically detect and hybridize. Therefore, claims 20-25, 27-30 are under examination. Claims 31-60 are withdrawn to inventions that lack unity of invention for reasons made of record.

The requirement is still deemed proper and is therefore made FINAL.

*Rejections Withdrawn*

The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

*Rejections Maintained*

Claims 20 and 21 stand rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention is maintained for reasons made of record for claim 1.

The amendment to the claims does not moot the rejection. As previously made of record, *Vas-Cath Inc. v. Mahurkar*, 19 USPQ2d 1111, 1117, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, *as of the filing date sought*, he or she was in possession *of the claimed invention*". "The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed* [emphasis added]". Therefore, Applicants' arguments are not persuasive. SEQ ID NO: 1 and 2 fragments of the p0157 plasmid of the prior art. No written description is provided in the specification for any other species of nucleic acids that are derived therefrom by mutation, deletion and/or substitution with the claimed function of specifically detecting enterohemorrhagic E. coli. The disclosure of a these discrete sequences (*which the claims are not limited toward*) does not reasonably constitute the claimed genus of nucleic hybridizing nucleic acids that are mutated, deleted or substituted in one or more bases. Analogous to the situation decided in *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993), "an adequate written description of a DNA [product] requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the DNA itself". *Fiddes v. Baird*, 30 USPQ2d 1481, 1483 (1993) held that claims directed to mammalian FGFs were found unpatentable due to lack of written

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description for the broad class, in which the specification had provided an adequate description of only the bovine sequence. Accordingly, the court held in *Univ. California v. Eli Lilly and Co.*, 43 USPQ2d 1398 (Fed. Cir. 1997) that: "One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is" and that: "A description of a genus of cDNAs [products] may be achieved by means of a recitation of a representative number of cDNAs [products], *defined by nucleotide sequence*, failing in the scope of the genus or of a recitation of structural features common to the members of the genus, *which features constitute a substantial portion of the genus* [emphasis added]. This is analogous to enablement of a genus under 112, [first paragraph], by showing the enablement of a representative number of species within the genus. See *Angstadt*, 537 F.2d at 502-03, 190 USPQ at 218". The specification does not teach any subsequence of either SEQ ID NO:1 or 2, that was derived by mutation, deletion and/or substitution of one or more bases. There is no written description for any sequences derived, much less those that would hybridize.

The rejection is maintained over the claimed sequences as "derived from SEQ ID NO:1 or 2 by mutation, deletion and/or substitution of one or more bases".

Claims 20, 21 and dependent claims 22-25 stand rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention is maintained for reasons made of record for the previous claims.

Applicants' arguments have been carefully considered. Applicants argue that representative examples of such high stringency conditions are recited in the specification. This is not persuasive, exemplification is not a definition of specific conditions and limitations as recited in the specification are not read into the claims.

Further, the conditions relied upon at page 7, lines 19-30 are admittedly specifically related to the specific chemical structure of the hybridizing nucleic acid, the structure of which is not defined in the claims. The rejection is therefore maintained.

Claims 20, 21, 22 and 24 stand rejected under 35 U.S.C. 102(b) as being clearly anticipated by Brunder et al (Microbiology, 146:3305-3315, 1996) for reasons made of record in the Office Action Mailed 12-13-03.

Applicants' arguments have been carefully considered but are not persuasive. Applicants argue that the inventors have demonstrated that *E. coli* 0157:7 is characterized by the stable integration of a portion of the *IS91* sequence into the *katP* gene. According the stable combination of a portion of *IS91* with a portion of *katP* is a specific marker for *E. coli* 0157:H7 strains. This is not persuasive, the claims are not so limited because "a portion" is a single "nucleotide" and the claims specifically encompass mutation, deletion or substitution of one or more bases or different ones and that the sequence of the prior art does not detect other EHEC's as set forth in the claims. The specific junction relied upon as set forth in the Figure is not defined in claim 21 and neither is the "portion" of sequence of *IS91* or "portion" of gene sequence of *katP*. Additionally, the "substitution could represent the substitution of "X" for "X + 12 or more additional bases". Further, plasmid pSm10 or pSM9 comprises the *Sma*-1 fragment of pO157 and contains more than 1 Kb upstream of the beginning of *katP* (see page 3307, Figure 1) as derived from of would specifically hybridize to SEQ ID NO:1, because as with SEQ ID NO:1 is derived from the 0157 enterohemorrhagic plasmid of the prior art. Further, the *Sma*-1 fragment inherently has the claimed nucleotide residues of claim 22. It is also noted that the first *HindIII* fragment of the *Sma*-1 fragment of pSm10 or pSmK9 as disclosed by Brunder et al would also inherently hybridize under the high stringency conditions and would be specific for the sequence that they were derived from. The specifically claimed nucleotide sequence is inherent to the plasmids. The art is applied

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against the nucleic acids of claims 24 and 25 because the claims are confusing as dependent from claims 20 and 21 respectively for reasons set forth in the second paragraph rejection above.

Claims 20, 21, 22, 24 and 25 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Makino et al , (DNA Research, 5(1):1-9, Feb 28, 1998) in light of GenEMBL Accession Number AB011549.

Makino et al teach the isolation of and complete nucleotide sequences of 93 kb and 3.3 kb plasmids of an enterohemorrhagic *Escherichia coli* O157:H7 derived from Sakai outbreak. Makino et al teach extraction of DNA from the bacterium and isolation of the pO157 plasmid and subsequent sequencing of the plasmid, see page 2, Materials and Methods. Makino et al teach that pO157 is represented by EMBL Accession Number AB011549 (page 2, column 2, second full paragraph). The isolated plasmid inherently characterized by the stable integration of a portion of the *IS91* sequence into the *katP* gene and inherently hybridizes under the asserted conditions because it is 99.2% identical as compared to SEQ ID NO:1 (see attached alignment). As previously set forth, the language of mutation, deletion and/or substitution of one or more bases specifically includes the differences between SEQ ID NO:1 and the plasmid of the art. The deletion of "insertion" does not remove the art because "mutation" or "substitution" as it is still recited in the claims, broadly encompasses substitutions, insertions and deletions. Mutations include deletions and substitutions base X could be X for X+1, 2, 3 nts... resulting in a substitution of a single base for multiple replacements or substitution of bases XYZ could be substituted with XZ resulting in the loss or addition of a single or multiple bases and the "consisting of language" does not limit the claims to shorter fragments because a nucleic acid that is larger can also specifically detect and hybridize. The isolated plasmid inherently hybridizes under stringent conditions because it comprises a sequence that is 98.7% identical as compared to SEQ ID NO:2 as evidenced by GenEMBL

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Accession Number ABO11549 (see attached alignment). Applicants argue that the sequence was not available prior to the priority date of this application. This is not persuasive, the filing date of the instant specification in the US is the instant filing date and the filing date of the international application is 4-27-1999. Applicants the priority document of 99/05329 filed 4-28-98 is in a foreign language and such the priority is not perfected. Even if the foreign priority is perfected, the paper was available as of February 29, 1998 and fully enabled as of this date. The nucleic acid sequence is inherent to the isolated plasmid. Claimed residues 400-407 of SEQ ID NO:1, SEQ ID NOS: 10-13, 18-20, 21-23 and 25 are inherently contained in the hybridizing plasmid of the prior art (see attached alignments for SEQ ID NOS:1 and 2).

#### *New Rejections Based on Amendment*

The amendment filed 7-12-04 is objected to under 35 U.S.C. 132(a) because it introduces new matter into the disclosure. 35 U.S.C. 132(a) states that no amendment shall introduce new matter into the disclosure of the invention. The added material which is not supported by the original disclosure is as follows: Applicants indicate a correction to the specification based on a foreign patent document of French origin. It is noted where a foreign priority document under 35 U.S.C. 119 is of record in the U.S. application file, applicant may not rely on the disclosure of that document to support correction of an error in the pending U.S. application. *Ex parte Bondiou*, 132 USPQ 356 (Bd. App. 1961). This prohibition applies regardless of the language of the foreign priority documents because a claim for priority is simply a claim for the benefit of an earlier filing date for subject matter that is common to two or more applications, and does not serve to incorporate the content of the priority document in the application in which the claim for priority is made. This prohibition does not apply where the U.S. application explicitly incorporates the foreign priority document by reference. Applicants have not provided for a specific incorporation by references in the originally filed transmittal documents or



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in the first line of the specification. As such, reliance on an incorporation by reference to correct the error is impermissible in this situation. Where a U.S. application as originally filed was in a non-English language and an English translation thereof was subsequently submitted pursuant to 37 CFR 1.52(d), if there is an error in the English translation, applicant may rely on the disclosure of the originally filed non-English language U.S. application to support correction of an error in the English translation document. In this case the originally filed document was not filed in a non-English language. Applicants are directed to MPEP section 2163.07 for correcting "obvious errors" not based on the priority documents.

Claims 20-25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The is a new matter rejection.

The claims now require the nucleic acid to "specifically detect" enterohemorrhagic *E. coli* wherein it is a fragment or derived from SEQ ID NO:1 that specifically detects enterohemorrhagic *E. coli* (EHECs) wherein the fragment or derived sequence contains a nucleotide sequence of SEQ ID NO:1 resulting from a stable combination of at least a portion of insertion sequence IS91 and at least a portion of gene sequence KatP. It is noted that the specification teaches that this portion 400-407 is *specific to 0157:H7* and does not detect other EHEC's (see page 5, lines 12-20) as it relates to claims 21, 22, 24 (SEQ ID NOS:12, 13, 18, 19 and 20). As such, the use of this junction that is specifically described in the specification as unique to 0157:H7, as an attribute of ECECs in general is considered new matter because the specification specifically teaches that it is not a genus marker.

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Claims 20-25 and 27-30 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

With respect to claims 20-25, the claims now recite that the isolated nucleic acid "specifically detect" enterohemorrhagic *Escherichia coli* (EHECs). In the absence of any definition in the specification, this phrase has been interpreted for this rejection as *exclusive detection of the target* (i.e. EHECs) to rule out detection of *all others*. The specification fails to disclose any individual/single isolated nucleic acid that specifically detects EHECs and some of the recited isolated nucleic acids are present in other genomes that are not EHEC's and an isolated nucleic acid consisting of SEQ ID NOS:10-13, 18-27 *per se* are of apparently insufficient length to form a stable hybrid under conditions such that they could *detect only EHECs* using single nucleic acid detection method such as hybridization. The specification is devoid of written description of specificity analysis with single nucleic acid probes for any of the particularly claimed nucleic acids. For example, with respect to specificity of detection using a single nucleic acid, residues 400-407 of SEQ ID NO:1 are present in fungi (see attached alignment) ; SEQ ID NO:19 is present in *Pseudomonas syringae* DNA for IS801 insertion sequence (see attached alignment) and SEQ ID NO:18 is present in *Salmonella paratyphi A* (see attached alignment) and porcine liver factor XII (see attached alignment) and therefore these nucleic acids are not specific as claimed and one would have reason to doubt the asserted truth that the others as specifically claimed are able to "specifically detect" detect EHECs as claimed. In the absence of further guidance from Applicants as to which single nucleic acids "specifically detect EHECs" as compared to other microorganism under which hybridization or other conditions. The primer pairs do not support the specific detection using a single nucleic acid. Primer pairs amplify a fragment that is specific and they

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themselves do not necessarily have to be exclusive. Therefore, the use of a specific primer pair to amplify a nucleic acid to generate a third nucleic acid sequence that has been identified as specific to 0157 is specifically distinguished from that which is claimed herein.

With respect to claims 27-30, Applicant's referral to the deposit of the clones pDF3 and pDF4 on page 5 of the specification is an insufficient assurance that all required deposits have been made and all the conditions of 37 CFR §1.801-1.809 have been met. If the deposit has been made under the provisions of the Budapest Treaty, filing of an affidavit or declaration by applicant or assignees or a statement by an attorney of record who has authority and control over the conditions of deposit over his or her signature and registration number stating that the deposit has been accepted by an International Depository Authority under the provisions of the Budapest Treaty, that all restrictions upon public access to the deposit will be irrevocably removed upon the grant of a patent on this application and that the deposit will be replaced if viable samples cannot be dispensed by the depository is required. This requirement is necessary when deposits are made under the provisions of the Budapest Treaty as the Treaty leaves this specific matter to the discretion of each State. *Amendment of the specification to recite the date of deposit and the complete name and full street address of the depository is required.* If the deposits *have not* been made under the provisions of the Budapest Treaty, then in order to certify that the deposits comply with the criteria set forth in 37 CFR §1.801-1.809, assurances regarding availability and permanency of deposits are required. Applicant's attention is directed to In re Lundack, 773 F.2d. 1216, 227 USPQ 90 (CAFC 1985) and 37 CFR §1.801-1.809 for further information concerning deposit practice.

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Claims 20, 21 and dependent claims 22-25 stand rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The claims now recite that the isolated nucleic acid "specifically detects" however, specificity is not defined in the specification nor is it defined as exclusive binding and therefore the metes and bounds of the claims can not be ascertained.

As to claims 22-25, the claims recite "the nucleic acid according to claim X" and it is not clear if the claims are intended to reference the "fragment" or "derived sequence". As such, it is not clear what alternative is specifically being limited in the dependent claims and therefore the dependent claims do not have proper antecedent basis or are properly dependent from independent claims 20 or 21.

As to claim 24, SEQ ID NOS:10 and 11, these sequences do not apparently have "at least a portion of IS91 and at least a portion of gene sequence katP, which appears to bridge residues 406-407 of SEQ ID NO:1 (see Figure 1). This issue is best resolved by Applicants pointing to the corresponding residues of each of these sequences that correspond to "the claimed "at least a portion of insertion sequence IS91" and "at least a portion of gene sequence katP".

Claims 20-25 are rejected under 35 U.S.C. 103(a) as being unpatentable over Makino et al , (DNA Research, 5(1):1-9, Feb 28, 1998) in view of Schmidt et al, Microbiology 142(4):907-914, 1996 and Kennell et al 1971( "Principles and properties of nucleic acid hybridization", Progr. Nucl. Acid Res. Mol. Biol. 11: 259-301) in light of GenEMBL Accession Number AB011549 .

Makino et al is set forth *supra*. Makino et al differs by not teaching fragments of SEQ ID NO:1 or SEQ ID NO:2. Kennel et al teach the location of the open reading frames in the sequenced p0157 plasmid, including the hly operon. Makino et al identifies

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the open reading frames of the junction of IS91/katP by nucleotide number and another open reading frame 82 corresponding to residues 87658-88761.

Schmidt et al teach that circular restriction fragment map of wild-type plasmid p0517 and location of the EHEC-hly operon (see page 910, Figure 2 and Table 1).

Kennell et al teach that nucleic acid sequences having a minimum size for stable complex formation is from 10-20 nucleotides depending upon the G+C content (see paragraph bridging pages 260-261).

It would have been *prima facie* obvious one of ordinary skill in the art at the time that the invention was made to use any restriction fragment of the p0157 plasmid of Schmidt et al of at least 10-20 nucleotides in length as a probe or primer to detect the p0157 of Makino et al or open reading fragment thereof because Makino et al teach that *E. coli* 0157:H7 is a pathogen that causes bloody diarrhea and hemorrhagic colitis and Kennel et al teach that the nucleic acids would form stable hybrids. To restate, any fragment of the p0157 plasmid from *E. coli* 0157:H7 having at least 10-20 nucleotides in length is *prima facie* obvious as a probe/primer for detecting the sequence of origin from enterohemorrhagic *E. coli* 0157:H7. The restriction fragment(s) would specifically detect the sequence from which it was derived. The art is applied against the nucleic acids of claims 24 and 25 because the claims are confusing as dependent from claims 20 and 21 respectively for reasons set forth in the second paragraph rejection above.

#### *Status of Claims*

All claims stand rejected.

#### *Conclusion*

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP

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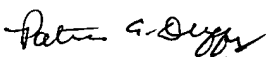
§ 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Patricia A. Duffy whose telephone number is 571-272-0855. The examiner can generally be reached on M-Th 6:30 am - 6:00 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith can be reached on 571-272-0864.

The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

  
Patricia A. Duffy

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Primary Examiner

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240 CGGCGCTGATACCGGCAAGATGTCGCAAACTCCGCTCCGTCAGCGGGCTATTTCAG 299  
 7076 CGGCGCTGATACCGGCAAGATGTCGCAAACTCCGCTCCGTCAGCGGGCTATTTCAG 7135  
 300 GATACCTTCGTCATCAACACGTCACAAACAGAGACACAGCTTTTGTGTTCTGACATCCA 359  
 7136 GATACCTTCGTCATCAACACGTCACAAACAGAGACACAGCTTTTGTGTTCTGACATCCA 7195  
 360 CAAAGAAGGGAATATTCAGGTCGTCGACAGCTCAACGCGCATCGTCAGTTGGCGCTTGA 419  
 7196 CAAAGAAGGGAATATTCAGGTCGTCGACAGCTCAACGCGCATCGTCAGTTGGCGCTTGA 7255  
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 7376 ATAAAAAACTCTCTGTTGATCTCTGCGCTATCGGGAGCTTTTCTACCGCT 7435  
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 KEYWORDS Escherichia coli  
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 ORGANISM Escherichia coli  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.  
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 AUTHORS Makino,K., Ishii,K., Yasunaga,T., Hattori,M., Yokoyama,K., Yutsudo,H.C., Kubota,Y., Yamauchi,Y., Iida,T., Yamamoto,K., Honda,T., Han,C.G., Ohtsuo,E., Kasamatsu,M., Hayashi,T., Kuhara,S. and Shinagawa,H.  
 TITLE Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic Escherichia coli O157:H7 derived from Sakai outbreak  
 JOURNAL DNA Res. 5 (1), 1-9 (1998)  
 MEDLINE 98290540  
 PUBMED 9628576  
 REFERENCE 2 (bases 1 to 92721)  
 AUTHORS Makino,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-FEB-1998) Kozo Makino, Research Institute for Microbial Diseases, Osaka University, Molecular Microbiology; Yamadaoka, 3-1, Suita, Osaka 562, Japan  
 COMMENT E-mail:makino@bks01.biken.osaka-u.ac.jp, Tel:81-6-879-8318, Fax:81-6-879-8320  
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Enterobacteriaceae; Escherichia.  
REFERENCE  
AUTHORS Iversen, P.L.  
TITLE Antisense antibacterial cell division composition and method  
JOURNAL Patent: WO 0149775-A 7 12-JUL-2001;  
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Db 87919 ATGGCAGATGACGATCAGGTTTAAATTTCCCGTAATCCGTCGAAGTCTGAGGATGA 87860  
QY 1091 AGGAAGGTGAAGGCTGTTCTGTAAGGAATAAAGTGAACATCATGCGCTTTTCTGGC 1150  
Db 87859 AGGAAGGTGAAGGCTGTTCTGTAAGGAATAAAGTGAACATCATGCGCTTTTCTGGC 87800  
QY 1151 TTCCGGAGCAATTTTACTTTTCTCTGCAG 1181  
Db 87799 TTCCGGAGCAATTTTACTTTTCTCTGCAG 87769

RESULT 9  
AF043470  
LOCUS AF043470 5612 bp DNA linear BCT 25-JUN-1998  
DEFINITION Escherichia coli plasmid pO157 ecf4 gene, partial cds; and ecf3, ecf2, and ecf1 genes, complete cds.  
ACCESSION AF043470  
VERSION AF043470.1 GI:3253288  
KEYWORDS  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
REFERENCE  
AUTHORS Boerlin, P., Chen, S., Colbourne, J.K., Johnson, R., De Grandis, S. and Gyles, C.  
TITLE Evolution of enterohemorrhagic Escherichia coli hemolysin plasmids and the locus for enterocyte effacement in shiga toxin-producing E. coli  
JOURNAL Infect. Immun. 66 (6), 2553-2561 (1998)  
MEDLINE 98261495  
PUBMED 9596716  
REFERENCE 2 (bases 1 to 5612)  
AUTHORS Boerlin, P. and Gyles, C.  
TITLE Direct Submission

Specificity

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source
1. .14
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Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTCAG 8
Db 11 ATCGTCAG 4

RESULT 7
LOCUS
DEFINITION
AR126298 14 bp DNA linear PAT 16-MAY-2001
ACCESSION
AR126298 Sequence 5 from patent US 6180339.
VERSION
AR126298.1 GI:14112891
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Sandhu,G.S. and Kline,B.C.
TITLE
Nucleic acid probes for the detection and identification of fungi
JOURNAL
Patent: US 6180339-A 5 30-JAN-2001;
FEATURES
Location/Qualifiers
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTCAG 8
Db 11 ATCGTCAG 4

RESULT 8
BD132864/c
LOCUS
DEFINITION
BD132864 Nucleic acid probes for the detection and identification of fungi.
ACCESSION
BD132864
VERSION
BD132864.1 GI:23227809
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Sandhu,G.S. and Kline,B.C.
TITLE
Nucleic acid probes for the detection and identification of fungi
JOURNAL
Patent: JP 2002504817-A 5 12-FEB-2002;
COMMENT
BAYER CORP
PN JP 2002504817-A/5
PD 12-FEB-2002
PF 04-JUN-1998 JP 1999501953
PI 06-JUN-1997 US 08/871678
PR GURPREET S SANDHU,BRUCE C KLINE
PC C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
1. .14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

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Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTCAG 8
Db 11 ATCGTCAG 4

RESULT 9
BD205228
LOCUS
DEFINITION
BD205228 Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC).
ACCESSION
BD205228
VERSION
BD205228.1 GI:33014998
KEYWORDS
JP 2002512813-A/18.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Frechon,D.T.M., Laure,F.C. and Thierry,D.
TITLE
Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC)
JOURNAL
Patent: JP 2002512813-A 18 08-MAY-2002;
COMMENT
BIORAD PASTEUR
OS Unidentified
PN JP 2002512813-A/18
PD 08-MAY-2002
PF 27-APR-1999 JP 2000546051
PR 28-APR-1998 FR 98/05329
PI DOMINIQUE THERESE MARIE FRECHON,FRANCOISE CLAUDINE LAURE, PI
PC C12N9/08,C07K14/245,C12N1/21,C12N15/09,C12Q1/68,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Nucleotide sequence for detecting enterohemorrhagic CC
Escherichia coli
(EHEC).
FH Key Location/Qualifiers
1. .14
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/mol_type="genomic DNA"
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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTCAG 8
Db 4 ATCGTCAG 11

RESULT 10
I79345/c
LOCUS
DEFINITION
I79345 Sequence 5 from patent US 5707802.
ACCESSION
I79345
VERSION
I79345.1 GI:3207635
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Sandhu,G.S. and Kline,B.C.
TITLE
Nucleic acid probes for the detection and identification of fungi
JOURNAL
Patent: US 5707802-A 5 13-JAN-1998;

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FEATURES
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    Location/Qualifiers
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ORIGIN
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  Best Local Similarity
    100.0%; Pred. No. 5.1e+05;
  Matches
    8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
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  |||||
Db
  11 ATCGTCAG 4

RESULT 11
AX011314
LOCUS
  AX011314
  14 bp DNA linear PAT 06-SEP-2000
DEFINITION
  Sequence 18 from Patent WO9955908.
ACCESSION
  AX011314
VERSION
  AX011314.1 GI:9997864
KEYWORDS
  Escherichia coli
SOURCE
  Escherichia coli
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.
REFERENCE
  1
  Thierry D., Frechon, D.T. and Laure, F.C.
  Nucleotide sequences for detecting enterohemorrhagic escherichia
  coli (ehc)
  PATENT: WO 9955908-A 18 04-NOV-1999;
  JOURNAL
  THIERRY DOMINIQUE (FR); FRECHON DOMINIQUE THERESE MARI (FR); LAURE
  FRANCOISE CLAUDE (FR); PASTEUR SANOFI DIAGNOSTICS (FR)
FEATURES
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    1..14
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    /db_xref="taxon:562"

ORIGIN
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  Best Local Similarity
    100.0%; Pred. No. 5.1e+05;
  Matches
    8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  1 ATCGTCAG 8
  |||||
Db
  4 ATCGTCAG 11

RESULT 12
AR301299/c
LOCUS
  AR301299
  15 bp DNA linear PAT 12-JUN-2003
DEFINITION
  Sequence 61 from patent US 6538122.
ACCESSION
  AR301299
VERSION
  AR301299.1 GI:31689072
KEYWORDS
  Unknown.
SOURCE
  Unknown.
  Organism
    Unclassified.
  1 (bases 1 to 15)
  Yokoyama, K., Nakamura, N., Miwa, T. and Seguro, K.
  Process for producing microbial transglutaminase
  PATENT: US 6538122-A 61 25-MAR-2003;
  JOURNAL
  Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
    1..15
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
  Query Match
    100.0%; Score 8; DB 6; Length 15;
  Best Local Similarity
    100.0%; Pred. No. 5.1e+05;
  Matches
    8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
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  |||||
Db
  10 ATCGTCAG 3

RESULT 13
AX103974/c
LOCUS
  AX103974
  15 bp DNA linear PAT 30-APR-2001
DEFINITION
  Sequence 166 from Patent WO0122972.
ACCESSION
  AX103974
VERSION
  AX103974.1 GI:13920171
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Krieg, A.M., Schetter, C. and Vollmer, J.C.
  Immunostimulatory nucleic acids
  PATENT: WO 0122972-A 166 05-APR-2001;
  JOURNAL
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
  GmbH (DE)
FEATURES
  source
    Location/Qualifiers
    1..15
    /organism="synthetic construct"
    /db_xref="taxon:32630"

ORIGIN
  Query Match
    100.0%; Score 8; DB 6; Length 15;
  Best Local Similarity
    100.0%; Pred. No. 5.1e+05;
  Matches
    8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  1 ATCGTCAG 8
  |||||
Db
  10 ATCGTCAG 3

RESULT 14
AX355608/c
LOCUS
  AX355608
  15 bp DNA linear PAT 06-FEB-2002
DEFINITION
  Sequence 636 from Patent WO0197843.
ACCESSION
  AX355608
VERSION
  AX355608.1 GI:18620276
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Weiner, G. and Hartmann, G.
  Methods for enhancing antibody-induced cell lysis and treating
  cancer
  PATENT: WO 0197843-A 636 27-DEC-2001;
  JOURNAL
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  source
    Location/Qualifiers
    1..15
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-phosphodiester backbone"

ORIGIN
  Query Match
    100.0%; Score 8; DB 6; Length 15;
  Best Local Similarity
    100.0%; Pred. No. 5.1e+05;
  Matches
    8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  1 ATCGTCAG 8
  |||||
Db
  10 ATCGTCAG 3

RESULT 15
AX547027/c
LOCUS
  AX547027
  15 bp DNA linear PAT 01-MAR-2003

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nd specific

RBS  
CDS  
misc\_feature  
ORIGIN

LAHTNGATLFTYLDHRTQAOQETLSQADMLFRVVQHIPEKHFRMIRYFGFLANRV  
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QGLNLQAQIAQMEYVKE"  
387...391  
/note="putative"  
complement(461..1060)  
/note="unnamed protein product;orf2"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="CAA40541.1"  
/db\_xref="GI:45832"  
/translation="MLFRDLVHHPKHVGLAQLFLLGLCAVIOVGEPQPGPVGMRO  
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1513..1517  
/note="insertion target sequence"  
/evidence=experimental

## ORIGIN

Query Match 100.0%; Score 14; DB 1; Length 1517;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCATCGTCAGTTG 14  
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Db 762 GGCATCGTCAGTTG 749

## RESULT 19

AB022426  
LOCUS AB022426 2055 bp mRNA linear MAM 21-JAN-1999  
DEFINITION Sus scrofa mRNA for FXII, complete cds.  
ACCESSION AB022426  
VERSION AB022426.1 GI:4165316  
KEYWORDS FXII.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

## REFERENCE

1 (bases 1 to 2055)  
Takahashi, T. and Kihara, T.  
Porcine liver factor XII  
Published Only in Database (1999)  
2 (bases 1 to 2055)  
Takahashi, T. and Kihara, T.  
Direct Submission  
Submitted (07-JAN-1999) Takayuki Takahashi, Hokkaido University,  
Graduate School of Science, Kitaku Kita 10 Joh Nishi 8 chome,  
Sapporo, Hokkaido 060-0810, Japan  
(E-mail:ttakahashi@sci.hokudai.ac.jp, Tel:81-11-706-2748,  
Fax:81-11-706-2748)

## FEATURES

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/organism="Sus scrofa"  
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/db\_xref="taxon:9823"  
/tissue type="liver"  
25..1875  
/codon\_start=1  
/product="FXII"  
/protein\_id="BAA37148.1"  
/db\_xref="GI:4165317"  
/translation="MRALLLIGLLVLSALLIPPWKDPRKHVMASEHTVTLVTG  
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PCOKGTGCVNMPGHCICPDHFTGKCHCKEKEFPQFPLOFQNEIWHRFEPAGVSK  
CCKGPKAQCKPVAQSVCSTNPLNGSCSLCTEGHRLCRCPTGAGLCVLDLKERCY  
SDRGLYKGMATQYLSCAPQWASEATTYNNATQALNWGLGHAFCRPNDDTRPW  
CFVWRGDLQWQYCLARCOAPIGEAPILPTQSPSEHSDPLSPREPQTTPTSQ  
NLTSACWAPPQPGVPLSAGVGGCQRLKRLSLNRIVGLVALPGAHPIYALYWG  
QNFCAGLSLIAFCWLVLTACLQNRPAPELTAVLIGQDRHNSCEQCOTLAVRSVLHE  
SYSPKTYQHDLLALVRLKETADGCCAHPSPFFVQVCLPRSVASSAEPGALCEVAGWGH

## CDS

ORIGIN  
QFEGAEYSSFLQEAQVPLISPERCSAADVHGAATPGMLCAGFLGGTACQGDSCG  
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Query Match 100.0%; Score 14; DB 4; Length 2055;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCATCGTCAGTTG 14  
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Db 1771 GGCATCGTCAGTTG 1784

RESULT 20  
AX073964/c  
LOCUS AX073964 5145 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 1 from Patent WO0104295.  
ACCESSION AX073964  
VERSION AX073964.1 GI:12710224

KEYWORDS  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
1  
Avides, M.D., Deak, P. and Glover, D.M.  
Orbit and homologues thereof.  
Patent: WO 0104295-A 1 18-JAN-2001;  
University of Dundee (GB)

FEATURES  
source  
1..5145  
/organism="Drosophila melanogaster"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:7227"

## ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 5145;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCATCGTCAGTTG 14  
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Db 3749 GGCATCGTCAGTTG 3736

RESULT 21  
AF195498/c  
LOCUS AF195498 5916 bp mRNA linear INV 01-NOV-2000  
DEFINITION Drosophila melanogaster clone L011488 Misexpression suppressor of  
ras 7 (MESR7) mRNA, MESR7-3403 allele, complete cds.

ACCESSION AF195498  
VERSION AF195498.1 GI:11066120  
KEYWORDS Full CDNA.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
1 (bases 1 to 5916)  
Huang, A.M., Rubin, G.M., Tsang, G., Evans-Holm, M. and Suh, C.  
Full length Drosophila melanogaster cDNA sequence  
Unpublished

2 (bases 1 to 5916)  
Huang, A.M., Rubin, G.M., Tsang, G., Evans-Holm, M. and Suh, C.  
Direct Submission  
Submitted (18-OCT-1999) Molecular and Cell Biology, University of  
California at Berkeley, 545 Life Sciences Addition Bldg., Berkeley,  
CA 94720-3200, USA

FEATURES  
source  
1..5916  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"



Mon Mar 14 11:04:16 2005

Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0; Mismatches 0; Matches 14; Conservative 0;

Qy 1 GGCATCGTCAGTTG 14  
Db 420 GGCATCGTCAGTTG 407

RESULT 2

US-10-282-122A-36930  
; Sequence 36930, Application US/10282122A  
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 36930

LENGTH: 1285

TYPE: DNA

ORGANISM: Salmonella paratyphi A

Query Match 100.0%; Score 14; DB 17; Length 1285;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0; Mismatches 0; Matches 14; Conservative 0;

Qy 1 GGCATCGTCAGTTG 14  
Db 403 GGCATCGTCAGTTG 416

RESULT 3

US-10-282-122A-40133  
; Sequence 40133, Application US/10282122A  
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangu

APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 40133

LENGTH: 1551

TYPE: DNA

ORGANISM: Salmonella typhi

US-10-282-122A-40133

Query Match 100.0%; Score 14; DB 17; Length 1551;

Best Local Similarity 100.0%; Pred. No. 4.4e+02; Indels 0; Gaps 0; Mismatches 14; Conservative 0;

Qy 1 GGCATCGTCAGTTG 14

Db 694 GGCATCGTCAGTTG 707

RESULT 4

US-09-738-626-1

; Sequence 1, Application US/09738626

; Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

LOCUS BD205211 1489 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC).  
ACCESSION BD205211  
VERSION BD205211.1 GI:33014981  
KEYWORDS JP 2002512813-A/1.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1489)  
AUTHORS Frechon,D.T.M., Laure,F.C. and Thierry,D.  
TITLE Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC)  
JOURNAL Patent: JP 2002512813-A 1 08-MAY-2002;  
COMMENT BIORAD PASTEUR  
OS Unidentified  
PN JP 2002512813-A/1  
PD 08-MAY-2002  
PF 27-APR-1999 JP 2000546051  
PR 28-APR-1998 FR 98/05329  
PI DOMINIQUE THERESE MARIE FRECHON, FRANCOISE CLAUDE LAURE, PI  
DOMINIQUE THIERRY  
PC C12N9/08, C07K14/245, C12N15/09, C12Q1/68, C12N15/00 CC  
Strandedness: Double;  
CC Topology: Linear;  
CC Nucleotide sequence for detecting enterohemorrhagic CC  
Escherichia coli  
(EHEC).  
CC Location/Qualifiers  
FH Key 1..1489  
FT source /organism='Unidentified'.  
FT Location/Qualifiers  
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1..1489  
/organism='unidentified'  
/mol\_type='genomic DNA'  
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ORIGIN  
Query Match 100.0%; Score 16; DB 6; Length 1489;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGCATCGTCAGTTCG 16  
DB 396 CGGCATCGTCAGTTCG 411  
RESULT 10  
LOCUS AX011297 1489 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 1 from Patent WO9955908.  
ACCESSION AX011297  
VERSION AX011297.1 GI:9997847  
KEYWORDS Escherichia coli  
SOURCE Escherichia coli  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.  
REFERENCE 1  
AUTHORS Thierry,D., Frechon,D.T. and Laure,F.C.  
TITLE Nucleotide sequences for detecting enterohemorrhagic escherichia coli (ehc)  
JOURNAL Patent: WO 9955908-A 1 04-NOV-1999;  
THIERRY DOMINIQUE (FR); FRECHON DOMINIQUE THERESE MARI (FR); LAURE FRANCOISE CLAUDE (FR); PASTEUR SANOFI DIAGNOSTICS (FR)  
FEATURES  
source  
1..1489  
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/db\_xref='taxon:562'  
ORIGIN  
Query Match 100.0%; Score 16; DB 6; Length 1489;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGCATCGTCAGTTCG 16  
DB 396 CGGCATCGTCAGTTCG 411  
RESULT 11  
LOCUS PS18801 1517 bp DNA linear BCT 07-JUL-2002  
DEFINITION P.syringae DNA for IS801 insertion sequence.  
ACCESSION X57269  
VERSION X57269.1 GI:45830  
KEYWORDS insertion element IS801.  
SOURCE Pseudomonas syringae  
ORGANISM Pseudomonas syringae  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.  
REFERENCE 1 (bases 1 to 1517)  
AUTHORS Romantschuk,M., Richter,G.Y., Mukhopadhyay,P. and Mills,D.  
TITLE IS801, an insertion sequence element isolated from Pseudomonas syringae pathovar phaseolicola  
JOURNAL Mol. Microbiol. 5 (3), 617-622 (1991)  
MEDLINE 91260445  
PUBMED 1646375  
REFERENCE 2 (bases 1 to 1517)  
AUTHORS Mills,D.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-1991) D. Mills, Oregon State University, Dept of Botany and Plant Pathology, Corvallis OR 97331-2902, U S A  
FEATURES  
source  
1..1517  
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/strain='pathovar phaseolicola, strain LR781'  
/db\_xref='taxon:317'  
misc\_feature 1..5  
/note='insertion target sequence duplication'  
evidence=experimental  
6..1512  
/insertion\_seq='IS801'  
101..1333  
/note='unnamed protein product; orf1'  
/codon\_start=1  
/transl\_table=1  
/protein\_id='CAA40540.1'  
/db\_xref='GI:45831'  
/db\_xref='GOA:P24607'  
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/translation='MKPAYPLLIQMSPAYTPRLKQLFTANQCWAHLLLEGGLRDIE VETVTKLAGCTSLGVKHYTCGNHSCPHVKYLCNTCHCRACPCGKATQWITVON NRPDPCWQHLVFTLPTLWPLFFYNWLLDALFLAADNLIYAKRRLRGVIFGAL HTYGRNLNHPHVLSTAGLDEQGVWKNLSFKKALRREWMVLRDYLGLQPSQL TMLPPLALICESDWRLLILAAGQGHWHILSKTKNGKTKVNLGRYLKPPISGR LAHTNGATLFTYLDHRTQYQOETLSQADMLFRVQHIPEKHFMRIRYFGFLANRV CGOYLKPYVEALKMATPGTPTKLYFAPMAKAFNLVDFPCVLCGARMVYTAISGLT QGLNLNAQAIQMEYVKE'  
387..391  
/note='putative'  
complement(461..1060)  
/note='unnamed protein product; orf2'  
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/db\_xref='UniProt/TREMBL:Q99178'  
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1513..1517  
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misc\_feature

/evidence-experimental

Query Match 100.0%; Score 16; DB 1; Length 1517;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATCGTCAGTTGC 16  
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Db 763 CGGCATCGTCAGTTGC 748

RESULT 12  
AY603980  
LOCUS AY603980  
DEFINITION Pseudomonas syringae pv. maculicola strain ES4326 plasmid  
ppMA4326B, complete sequence.  
ACCESSION AY603980  
VERSION AY603980.1 GI:47525154  
KEYWORDS Pseudomonas syringae pv. maculicola  
SOURCE Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
ORGANISM  
1 (bases 1 to 40110)  
Stavrinides, J. and Guttman, D.S.  
REFERENCE Nucleotide Sequence and Evolution of the Five-Plasmid Complement of  
the Phytopathogen Pseudomonas syringae pv. maculicola ES4326  
J. Bacteriol. 186 (15), 5101-5115 (2004)  
15262947  
2 (bases 1 to 40110)  
Stavrinides, J.  
REFERENCE Direct Submission  
AUTHORS Submitted (21-APR-2004) Department of Botany, University of  
Toronto, 25 Willcocks Street, Toronto, ON M5S3B2, Canada  
JOURNAL Location/Qualifiers  
FEATURES  
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/genes="repA"  
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1..1302  
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plasmid pDC3000A replication protein RepA encoded by  
GenBank Accession Number AE016855"  
/codon\_start=1  
/transl\_table=11  
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/protein\_id="AAT35168.1"  
/db\_xref="GI:47525155"  
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PAPLMVRKSHGSLFYAVSPVCTENAPKQVYVDFDHDHANALWDAGL  
PVAKTPHWETTESHYVELGELASAVELTVPWATGPKLDQVSHRHGILFEOL  
RYFAYSIVNRELGSPFSFMRSLDAYAVNHNHSLKQGFSENLPLSSIRATVKSVRW  
TWDRYTGDRCHRGAMQLDSSLTERQSLAARRTHELRHAKATESKIRACRQLODQG  
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1451..1744  
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GenBank Accession Number AE016860"  
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1816..2016  
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1816..2016  
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/note="similar to Escherichia coli O157:H7 EDL933 unknown  
protein encoded by cryptic prophage CP-933P encoded by  
GenBank Accession Number AE006461; possible  
post-segregational killing system"  
/codon\_start=1  
/transl\_table=11  
/product="stability determinant"  
/protein\_id="AAT35170.1"  
/db\_xref="GI:47525157"  
/translation="MEKILMIDRSPIVSEFETEELNAYTALRAKVEASLADSRPAI  
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2016..2309  
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2016..2309  
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(pPAM05016); possible post segregational killing system"  
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/db\_xref="GI:47525158"  
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3001..5096  
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3181..4741  
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AF359557; insertion caused disruption and frameshift in  
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complement(5094..5256)  
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DC3000 ISPaay transposase encoded by GenBank Accession  
Number AE016867"  
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5391..6809  
/locus\_tag="PMA4326B06"  
5391..6809

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FDPAINVHARSGLRRMPVLLRRRAIDALQGLCFHYDPLANRVQCSTTLAIECG
LATSAAGKLSITRAYNTALFELGILITVOTEDPLIGCYIPTDITFTPALPAALDV
SEDAVAAGRSRVENRNLAKQGLDTLGNDELIAKAWRFRFRSYQTELKSGIK
RARADAGRRQDITLVLRQKUTREISEGRFTANREAVKREVRKEMILLNRN
YSRLATASP"
misc_feature
3847..4095
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/notes="88 pct identical to locus ECCIS accession X12587,
required for cis-activation of oriR by the replication
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4072..4080
/notes="dnaA site; 100 pct identical (0 gaps) to locus
ECNR1REP at (1682..1690) accession X02302"
4084..4232
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segment for replication of E. coli IncFII plasmid NR1
ECREP1 X12776"
/direction=right
promoter
4169..4197
/notes="predicted sigma 70 promoter; score of 56%"
4259..4453
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Query Match 100.0%; Score 26; DB 1; Length 92077;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGGTTCCAGCGCAACTGACGA 26
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Db 7262 AAGGGTTCCAGCGCAACTGACGA 7237
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RESULT 6
AX191727/c
LOCUS AX191727 92077 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 9 from Patent WO0149775.
ACCESSION AX191727
VERSION AX191727.1 GI:15209896
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
1 Iversen,P.L.
Antisense antibacterial cell division composition and method
Patent: WO 0149775-A 9 12-JUL-2001;
Avi Biopharma, Inc. (US)
LOCATION/Qualifiers
1..92077
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
ORIGIN
Query Match 100.0%; Score 26; DB 6; Length 92077;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGGTTCCAGCGCAACTGACGA 26
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Db 7262 AAGGGTTCCAGCGCAACTGACGA 7237
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RESULT 7
AB011549/c
LOCUS AB011549 92721 bp DNA circular BCT 27-APR-1999
DEFINITION Escherichia coli plasmid pO157 DNA, complete sequence.
ACCESSION AB011549
VERSION AB011549.2 GI:4589740
KEYWORDS ToxR-regulated lipoprotein; tagA.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
1 (sites)
Makino,K., Ishii,K., Yasunaga,T., Hattori,M., Yokoyama,K.,
Yutsudo,H.C., Kubota,Y., Yamaichi,Y., Iida,T., Yamamoto,K.,
Honda,T., Han,C.G., Ohtsubo,E., Kasamatsu,M., Hayashi,T., Kuhara,S.
and Shinagawa,H.
Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
outbreak
DNA Res. 5 (1), 1-9 (1998)
98290540
9628576
REFERENCE 2 (bases 1 to 92721)
Makino,K.
Direct Submission
Submitted (24-FEB-1998) Kozo Makino, Research Institute for
Microbial Diseases, Osaka University, Molecular Microbiology;
Yamadaoka, 3-1, Suita, Osaka 562, Japan
(E-mail:makino@bks01.biken.osaka-u.ac.jp. Tel:81-6-879-8318,
Fax:81-6-879-8320)
On Apr 20, 1999 this sequence version replaced gi:3336997.
COMMENT
LOCATION/Qualifiers
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/mol_type="genomic DNA"
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/sub_strain="RIMD 0509952"
/db_xref="taxon:562"
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coli, EHEC O157:H7"
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join(92527..92721,1..2502)
/genes="tagA"
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KLSADSGSSIHSLTNALVEIHTANGRWVVDIYLPQGPDLGKVMRFVSSAGYSSTV
FYGDKVTLISVGNLTLPKYVNGWFRSGELENRIITYAOHWSAELPAHWIVPGLNLV
IKQNLISGLNDIKIGAPGELLHTIDIGMLTTPDRDFDPAKDKAEHREYFOTIPVSR
MIVNTAPHLKEMLPTEGELLTMDPFGCGWHSCTNRQRIKELVSHGIDNANYGLN
STAGLGNSHPYVVAQAAHNSNGYANGIQVHGGGGGIVTLDSLTGNEFSHEVGH
NYGLGHYVDGFGKSVHRSANNNTWGDGKKRFTPNFYPSQTNEKSCLNQCQBP
DGHKFGDAMAGSPFSAANFTMYTPNSAIIRPENKAVFDSRSSTGFSKNADT
QEMPEYHTIDRAEQITASVNELSEKMAELMAEYAVVVMWNGWNTRIYIPTASA
DNRSILITINHEAGYSYLFINGDEKVSQYKSFVSDQGFWRKRDVDTREARKPE
QFGVPVTLVGYDDPPELTSSYIYPAMYGAIFTYSDDSNLSDNDQLQVDTKEGQL
RFLRANRANTVMNFKNINPTESQPTQATLVNKNKILDTKSLTTPAPEGLUTYVNGQ
ALPAKENEGCIVSNGSKRCFLPVGQSGYSLPDWIVGQEVYVDGAKAVKLLSDWDN
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2589..3464
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Db 7263 TAAGGGTTCCAAAGCGCAACTGACG 7238

RESULT 7

AB011549/c

LOCUS

DEFINITION

AB011549

ACCESSION

AB011549.2

VERSION

GI:4589740

KEYWORDS

ToxR-regulated lipoprotein; tagA.

SOURCE

Escherichia coli

ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE

1 (sites)

Makino, K., Ishii, K., Yasunaga, T., Hattori, M., Yokoyama, K., Yutsudo, H.C., Kubota, Y., Yamauchi, Y., Iida, T., Yamamoto, K., Honda, T., Han, C.G., Ohtsubo, E., Kasamatsu, M., Hayashi, T., Kuhara, S. and Shinagawa, H.

TITLE

Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic Escherichia coli O157:H7 derived from Sakai outbreak

JOURNAL

DNA Res. 5 (1), 1-9 (1998)

MEDLINE

98290540

PUBMED

9628576

REFERENCE

2 (bases 1 to 92721)

Makino, K.

AUTHORS

Direct Submission

TITLE

Submitted (24-FEB-1998) Kozo Makino, Research Institute for Microbial Diseases, Osaka University, Molecular Microbiology; Yamadaoka, 3-1, Suita, Osaka 562, Japan

JOURNAL

(E-mail: makino@bks01.biken.osaka-u.ac.jp, Tel: 81-6-879-8318, Fax: 81-6-879-8320)

COMMENT

On Apr 20, 1999 this sequence version replaced gi:3336997.

FEATURES

Location/Qualifiers

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/mol\_type="genomic DNA"

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/sub\_strain="RIMD 0509952"

/db\_xref="taxon:562"

/plasmid="pO157"

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join(92527..92721,1..2502)

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/transl\_table=11

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/protein\_id="BAA31757.3"

/db\_xref="GI:4666293"

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gene

CDS

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3847..4095

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misc\_feature

4072..4080

/note="dnaA site; 100 pct identical (0 gaps) to locus ECNR1REP at (1682..1690) accession X02302"

rep\_origin

4084..4232

/standard\_name="oriR"

/note="89 pct identical to oriR (1094..1242); minimum segment for replication of E. coli IncFII plasmid NR1 ECRP4L X12776"

/direction="right"

promoter

4169..4197

/note="predicted sigma 70 promoter; score of 56"

gene

4259..4453

/gene="L7009"

CDS

4259..4453

/gene="L7009"

/note="95 pct identical to (0 gaps) 64 residues of a 128 aa protein REPA4 locus ECRSCL accession V00351"

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Query Match 100.0%; Score 26; DB 1; Length 92077;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAGGGTTCCAAAGCGCAACTGACG 26

Db 7263 TAAGGGTTCCAAAGCGCAACTGACG 7238

RESULT 6

AX191727/c

LOCUS

DEFINITION

Sequence 9 from Patent WO0149775.

ACCESSION

AX191727

VERSION

AX191727.1

KEYWORDS

GI:15209896

SOURCE

Escherichia coli

ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE

1

Iversen, P.L.

AUTHORS

Antisense antibacterial cell division composition and method

TITLE

Patent: WO 0149775-A 9 12-JUL-2001;

JOURNAL

Avi Biopharma, Inc. (US)

FEATURES

Location/Qualifiers

1..92077

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/mol\_type="unassigned DNA"

/db\_xref="taxon:562"

source

100.0%; Score 26; DB 6; Length 92077;

Query Match 100.0%; Pred. No. 0.12;

Best Local Similarity 100.0%;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAAGGGTTCCAAAGCGCAACTGACG 26

1026)

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LQAKWDGYTAETIAKQILQRQSPKTHLQNAQASRPETRGDVGQY
CFNLAINVGVVDLTSIPYAARIFQOLLINQVELLQARQVTAALRDWIDRDD
GAEDSVYMGMEPPYLAANQPMQDVSELRIGIDARLYRKLIPYVCVLPISDL
TLLDSQAPLALFLTKPDSLPTVTELLQRPRGTGWESVAFLDAPLKDIDTS
LAVSSNYFLVRLLHVSQGLHFSQQLMQWRERFRRIQRQYGLTMRQVP"
11473..12321

gene
Query Match 100.0%; Score 16; DB 1; Length 92721;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CGGCATCGTCAGTTGC 16
DB 76747 CGGCATCGTCAGTTGC 76762

RESULT 16
AX191725
LOCUS AX191725 92721 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 7 from Patent WO0149775.
ACCESSION AX191725
VERSION AX191725.1 GI:15209894
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1
Iversen,P.L.
AUTHORS Antisense antibacterial cell division composition and method
TITLE Patent: WO 0149775-A 7 12-JUL-2001;
JOURNAL Avi Biopharma, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CGGCATCGTCAGTTGC 16
DB 76747 CGGCATCGTCAGTTGC 76762

RESULT 17
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LOCUS UBA319838 536 bp DNA linear BCT 27-SEP-2000
DEFINITION Uncultured bacterium SB-53-TW partial 16S rRNA gene.
ACCESSION AJ319838
VERSION AJ319838.1 GI:21489345
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
1
Schaefer,H., Abbas,B., Witte,H. and Muyzer,G.
AUTHORS Genetic diversity of 'satellite' bacteria present in cultures of
TITLE marine diatoms
JOURNAL FEMS Microbiol. Ecol. 42 (1), 25-35 (2002)
REFERENCE 2 (bases 1 to 536)
AUTHORS Schaefer,H.
TITLE Direct Submission

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AF074613 92077 bp DNA circular BCT 04-NOV-1998  
 DEFINITION Escherichia coli O157:H7 plasmid pO157, complete sequence.  
 ACCESSION AF074613  
 VERSION AF074613.1 GI:3822114  
 KEYWORDS  
 SOURCE Escherichia coli O157:H7  
 ORGANISM Escherichia coli O157:H7  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Escherichia.  
 1 (bases 1 to 92077)  
 BURLAND,V., Shao,Y., Perna,N.T., Plunkett,G., Sofia,H.J. and  
 Blattner,F.R.  
 The complete DNA sequence and analysis of the large virulence  
 plasmid of Escherichia coli O157:H7  
 Nucleic Acids Res. 26 (18), 4196-4204 (1998)  
 98391744  
 PubMed 972640  
 2 (bases 1 to 92077)  
 BURLAND,V., Shao,Y., Perna,N.T., Plunkett,G. III, Sofia,H.J. and  
 Blattner,F.R.  
 Direct Submission  
 Submitted (25-JUN-1998) Genetics, University of Wisconsin, 445  
 Henry Mall, Madison, WI 53706, USA  
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 gene  
 CDS  
 promoter  
 gene  
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 gene  
 CDS



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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGCATCGTCAGTTGCG 18
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Db 7231 ACGGCATCGTCAGTTGCG 7248

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AB011549 92721 bp DNA circular BCT 27-APR-1999
DEFINITION
Escherichia coli plasmid p0157 DNA, complete sequence.
ACCESSION
AB011549
VERSION
AB011549.2 GI:4589740
KEYWORDS
ToxR-regulated lipoprotein; tagA.
SOURCE
Escherichia coli
ORGANISM
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
AUTHORS
Makino,K., Ishii,K., Yasunaga,T., Hattori,M., Yokoyama,K.,
Yutsudo,H.C., Kubota,Y., Yamaichi,Y., Iida,T., Yamamoto,K.,
Honda,T., Han,C.G., Ohtsubo,E., Kasamatsu,M., Hayaashi,T., Kuhara,S.
and Shinagawa,H.
Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
outbreak
DNA Res. 5 (1), 1-9 (1998)
98290540
PUBMED
9628576
REFERENCE
2 (bases 1 to 92721)
Direct Submission
AUTHORS
Makino,K.
TITLE
Submitted (24-FEB-1998) Kozo Makino, Research Institute for
Microbial Diseases, Osaka University, Molecular Microbiology;
Yamadaoka, 3-1, Suita, Osaka 562, Japan
(E-mail:makino@bks01.biken.osaka-u.ac.jp, Tel:81-6-879-8318,
Fax:81-6-879-8320)
On Apr 20, 1999 this sequence version replaced gi:3336997.
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CDS
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/notes="88 pct identical to locus ECCIS accession X12587,
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segment for replication of E. coli IncFII plasmid NR1
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/direction=right
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/notes="predicted sigma 70 promoter; score of 56%"
4259..4453
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aa protein REPA4 locus ECHSC1 accession V00351"
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Query Match 100.0%; Score 18; DB 1; Length 92077;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGCATCGTCAGTTGCG 18
|||||
Db 7231 ACGGCATCGTCAGTTGCG 7248

RESULT 10
LOCUS
AX191727 92077 bp DNA linear PAT 15-AUG-2001
DEFINITION
Sequence 9 from Patent WO0149775.
ACCESSION
AX191727
VERSION
AX191727.1 GI:15209896
KEYWORDS
Escherichia coli
SOURCE
Escherichia coli
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